



IN THE CLAIMS

In the claims, please cancel Claims 1 through 25. Please add Claims 26 through 47. A clean version of all of the claims is included below. Please add the claims:

26. (NEW) A method for eliminating redundant sequences that are common between two samples, the method comprising of the steps:
- isolating RNA strands from a first sample;
 - isolating RNA strands from a second sample;
 - generating cDNA strands from the RNA strands from the first sample;
 - mixing the cDNA strands of the first sample with the RNA strands from the second sample, the cDNA strands and RNA strands with common sequences hybridizing to form cDNA/RNA compliments; and
 - degrading the compliments.
27. (NEW) The method of Claim 26, wherein the step of generating cDNA strands for the RNA strands from the first sample comprises performing RT-PCR.
28. (NEW) The method of Claim 27, wherein the step of performing RT-PCR utilizes radioactive labeled to anchored oligo dT primers.
29. (NEW) The method of Claim 26, wherein the first sample is a healthy tissue and the second sample is a diseased tissue.
30. (NEW) The method of Claim 26, wherein the first sample is a diseased tissue and the second sample is a healthy tissue.
31. (NEW) The method of Claim 26, further comprising:
- amplifying the unhybridized cDNA strands using PCR.
32. (NEW) The method of Claim 26, further comprising:
- producing a second set of cDNA strands from unhybridized RNA strands.
33. (NEW) The method of Claim 32, further comprising:
- amplifying the second set of cDNA strands using PCR.

34. (NEW) The method of Claim 26, wherein the step of degrading compliments is performed with an Exonuclease III enzyme.

35. (NEW) The method of Claim 26, wherein the step of degrading compliments is performed with an Exonuclease IV enzyme.

36. (NEW) The method of Claim 26, further comprising:
displaying the unhybridized cDNAs or RNAs

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37. (NEW) The method of Claim 36, wherein the step of displaying comprises using electrophoresis.

38. (NEW) The method of Claim 26, further comprising:
reading the unhybridized cDNA strands or RNA strands with a photographic plate.

39. (NEW) The method of Claim 26, wherein the first and second samples are selected from a group comprising cells, tissues, pathogens, plants, and animals.

40. (NEW) The method of Claim 26, wherein the first and second sample are differentiated due to a diseased state, developmental, change, or induced by an external or internal stimulus.

41. (NEW) A method for determining differences between a first sample of cDNA strands and a second sample of RNA strands, the method comprising of the steps:
mixing the first sample of cDNA strands with the second sample of RNA strands,
the cDNA strands and RNA strands with common sequences hybridizing to
form cDNA/RNA compliments; and
degrading the cDNA/RNA compliments.

42. (NEW) The method of Claim 41, wherein the first sample of cDNA strands are produced from a third sample of RNA strands using RT-PCR utilizes radioactive labeled to anchored oligo dT primers.

43. (NEW) The method of Claim 41, further comprising:
amplifying unhybridized cDNA strands using PCR.

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44. (NEW) The method of Claim 41, further comprising:
producing a further set of cDNA strands from unhybridized RNA strands.

45. (NEW) The method of Claim 44, further comprising:
amplifying the further set of cDNA strands using PCR.

46. (NEW) The method of Claim 41, wherein the step of degrading compliments is performed with an Exonuclease III enzyme.

47. (NEW) The method of Claim 41, wherein the step of degrading compliments is performed with an Exonuclease IV enzyme.
